



STIC Search Report

Biotech-Chem Library

File Copy
09/903, 508
updated

STIC Database Tracking Number: 139815

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Wednesday, December 08, 2004

Case Serial Number: 09/903508

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:15:48 ; Search time 379 Seconds

(without alignments)
6745.298 Million cell updates/sec

Title: US-09-903-508A-3

Perfect score: 487

Sequence: 1 ttgattacgaattcgagctgg.....agtttcattgattctgttta 487

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	99.8	487	6 AAL41986	Aal41986 Candida f
2	457	93.8	1493	6 AAL41984	Aal41984 Candida f
3	206	42.3	827	6 ABS63000	ABS63000 Selected
4	206	42.3	827	6 ABT11605	ABT11605 Yeast sel
5	206	42.3	11198	4 AAD07496	Aad07496 PYLR110P
6	206	42.3	11201	4 AAD07498	Aad07498 PYMR107P
7	206	42.3	11204	4 AAD07499	Aad07499 PZEO1P DN
8	206	42.3	11427	4 AAD07497	Aad07497 PYMR251AP
9	206	42.3	12008	4 AAD07500	Aad07500 PP1BP DN
10	206	42.3	12844	4 AAD07492	Aad07492 PYLR110P+
11	206	42.3	12850	4 AAD07495	Aad07495 PZEO1P+lu
12	206	42.3	12851	4 AAD07494	Aad07494 PYMR107P+
13	206	42.3	13073	4 AAD07493	Aad07493 PYMR251AP
14	206	42.3	13654	4 AAD07501	Aad07501 PP1BP+lu
15	189.8	39.0	8800	6 ABK95584	ABK95584 Yeast rep
16	189.8	39.0	10042	6 ABK95585	ABK95585 Yeast rep
17	188.4	38.7	11365	6 ABK87505	ABK87505 Directed
18	177.8	36.5	7429	10 ADD02778	Add02778 Plasmid p
19	177.8	36.5	11713	3 AC55501	Ac55501 Destinati
20	177.8	36.5	12888	3 AC55629	Ac55629 Destinati
21	176.2	36.2	9952	10 ABV77349	ABV77349 Yeast exp

22	120	24.6	1494	8 AAD48348	Aad48348 Saccharom
23	84.8	17.4	10213	10 ADD02779	Add02779 Plasmid p
24	73.2	15.0	5161	4 AAF61508	Aaf61508 A. Gossyp
25	71	14.6	1467	6 ABZ31929	Abz31929 Candida a
26	70.6	14.5	1473	10 ADF5062	Adf5062 A. Gossyp
27	60.2	12.4	5615	11 ADM47088	Adm47088 Ogatea m
28	53	10.9	1554	8 ABT20720	Abt20720 Aspergill
29	53	10.9	1778	8 ABT20122	Abt20122 Aspergill
30	53	10.9	3140	8 ABT17712	Abt17712 Aspergill
31	53	10.9	3778	8 ABT19526	Abt19526 Aspergill
32	52.6	10.8	10250	6 ABN80083	Abn80083 Human che
33	51.4	10.6	76	12 ADM98299	Adm98299 PCR prime
34	51.2	10.5	2486	3 AA97037	Aa97037 Nucleotid
35	50.4	10.3	1373	2 AAV52969	Aav52969 Human G1
36	50.2	10.3	29993	10 ADB37662	Adb37662 Human che
37	50.2	10.3	29993	10 ADB37660	Adb37660 Human che
38	50.2	10.3	38342	4 AAS46745	Aas46745 Tumour su
39	50.2	10.3	38342	6 ABK31506	Abk31506 Signal tr
40	50	10.3	123	2 AAX87476	Aax87476 Plasmid p
41	50	10.3	6236	6 ABL33631	AbL33631 Human imm
42	50	10.3	6236	6 ABN80203	Abn80203 Human che
43	50	10.3	110000	2 AAT42063_03	Continuation (4 of
44	47.8	9.8	61020	4 AAS46787	Aas46787 Tumour su
45	47.6	9.8	7047	6 ABK28386	Abk28386 DNA trans

ALIGNMENTS..

RESULT 1
AAL41986
ID AAL41986 standard; DNA; 497 BP.
XX
AC AAL41986;
XX
DT 29-AUG-2003 (revised)
DT 13-MAY-2002 (first entry)
XX
XX Candida famata VKM Y-9 ARS element (CfARS) 2.

XX VKM T-9 ARS element; ds; autonomous replicating sequence element; CfARS;
KW flavinogenic yeast transformation; electroporation;
KW yeast cell spheroplast.
XX
XX Debaryomyces hansenii.
XX
XX WO200206448-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 13-JUL-2001; 2001WO-US022083.
XX

PR 14-JUL-2000; 2000US-0218244P.
PR 04-MAY-2001; 2001US-0288491P.
PR 15-MAY-2001; 2001US-0290667P.
PA (ABBA/) ABBAS C.
XX
PI Abbas C;
XX
XX WPI; 2002-148374/19.
DR
XX A nucleic acid construct used in the transformation of the flavinogenic
PT Yeasts Pichia guilliermondii and Candida famata by electroporation and
PT spheroplast formation.
PT
PT Claim 2; Fig 20; 202pp; English.

CC The invention comprises the nucleotide sequences of three autonomous
CC replicating sequence (ARS) elements. The invention also comprises methods
CC for the transformation of yeast cells (e.g. flavinogenic yeast). One such
CC method involves electroporating a yeast cell suspension, together with
CC constructs containing the ARS elements of the invention. Another yeast

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OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 20:18:39 ; Search time 78 Seconds
(without alignments)
4437.874 Million cell updates/sec

Title: US-09-903-508A-3
Perfect score: 487
Sequence: 1 tgcatacgaatcgagctcg.....agtttcgatgatttctgtta 487

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/1/ina/5A COMB.seq: *
4: /cgn2_6/ptodata/1/ina/5B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	43.3	8001	US-09-765-298A-39	Sequence 29, Appl
2	206	42.3	11198	US-09-743-194-23	Sequence 23, Appl
3	206	42.3	11201	US-09-743-194-25	Sequence 25, Appl
4	206	42.3	11204	US-09-743-194-26	Sequence 26, Appl
5	206	42.3	11427	US-09-743-194-24	Sequence 24, Appl
6	206	42.3	12008	US-09-743-194-27	Sequence 27, Appl
7	206	42.3	12844	US-09-743-194-19	Sequence 19, Appl
8	206	42.3	12850	US-09-743-194-22	Sequence 22, Appl
9	206	42.3	12851	US-09-743-194-21	Sequence 21, Appl
10	206	42.3	13073	US-09-743-194-20	Sequence 20, Appl
11	206	42.3	13654	US-09-743-194-28	Sequence 28, Appl
12	71	14.6	279	US-09-248-796A-3557	Sequence 3557, Ap
13	50	10.3	1830121	US-09-557-884-1	Sequence 1, Appl
14	50	10.3	1830121	US-09-643-990A-1	Sequence 1, Appl
15	50	10.3	1830121	US-10-329-960-1	Sequence 1, Appl
16	48	9.9	1141	US-09-806-708B-22	Sequence 22, Appl
17	46	9.4	6124	US-08-213-419B-3	Sequence 3, Appl
18	44.6	9.2	1493	US-08-340-820-24	Sequence 24, Appl
19	44.6	9.2	1493	US-08-593-535-24	Sequence 24, Appl
20	44.6	9.2	5152	US-10-204-708-73	Sequence 73, Appl
21	44.4	9.1	731	US-08-451-405A-2	Sequence 2, Appl
22	43	8.8	1850	US-08-617-860B-32	Sequence 32, Appl
23	43	8.8	4098	US-08-605-106-4	Sequence 4, Appl
24	42.6	8.7	640881	US-09-790-988-1	Sequence 1, Appl
25	42.2	8.7	832	US-09-621-976-2813	Sequence 2813, Ap
26	42.2	8.7	2434	US-09-489-847-67	Sequence 67, Appl
27	42.2	8.7	3165	US-09-601-198-102	Sequence 102, App

ALIGNMENTS

RESULT 1
US-09-765-298A-29
; Sequence 29, Application US/09765298A
; Patent No. 6582927
; GENERAL INFORMATION:
; APPLICANT: ARONHEIM, AMI
; TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT THI
; FILE REFERENCE: 108387.01
; CURRENT APPLICATION NUMBER: US/09/765,298A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: IL 125456
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: IL 128017
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-298A-29

Query Match	43.3%	Score 211;	DB 4;	Length 8001;
Best Local Similarity	78.1%	Pred. No. 6.8e-37;		
Matches	253;	Conservative	0;	Mismatches 71; Indels 0; Gaps 0;
Qy	164	TCATACCAATTAAGAACAACTTAAAGTCACATATGACAAATTCAGAAATACAAATCGATG	223	
Db	2701	TGAACGCCAAGGATTGATATGATATGATGATCAATGAATTAACATATATAAAATGATGAT	2760	
Qy	224	ATCCGTCATGATAAGCTGCAAGTCAACAGGCTAACTAAGATCCCTCTAGAGTC	283	
Db	2761	AATAATTTATAGATTTGTTAGATTTGAGATTCCTTTTATGGATTCCTAAATCCTC	2820	
Qy	284	GACTACGTCGTTAAGCCCGTTTCTGACAGAGTAAATTTTGAGGGAATTTACACATTA	343	
Db	2821	GACTACGTCGTTAAGCCCGTTTCTGACAGAGTAAATTTCTGAGGGAATTTTACACATTA	2880	
Qy	344	TGGGAATGCTTCAAGAGGATTTGACTTTAACTCCATCAATGTCAGGTCATTCAGTG	403	
Db	2881	TGGGAATGCTTCAAGAGGATTTGACTTTAACTCCATCAATGTCAGGTCATTCAGTG	2940	
Qy	404	TTTTTTATTGTTGTTATTTTTTTTTTTTAGAGAAAATCCTCAATATATAAATAGGAA	463	
Db	2941	TTTTTTATTGTTGTTATTTTTTTTTTTTAGAGAAAATCCTCAATATATAAATAGGAA	3000	
Qy	464	TCATAGTTTCATGATTTTCTGTTA	487	
Db	3001	TCATAGTTTCATGATTTTCTGTTA	3024	

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OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 21:19:17 ; Search time 385 Seconds

(without alignments)
6950.904 Million cell updates/sec

Title: US-09-903-508A-3

Perfect score: 487
Sequence: 1 tgatagaattcagctcg.....agtttcattgatttcgttta 487

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09D_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	99.8	487	10	US-09-903-508A-3
2	457	93.8	1493	10	US-09-903-508A-1
3	211	43.3	8001	9	US-09-765-298A-29
C 4	206	42.3	11198	17	US-10-776-213-23
C 5	206	42.3	11201	17	US-10-776-213-25
C 6	206	42.3	11204	17	US-10-776-213-26
C 7	206	42.3	11427	17	US-10-776-213-24
C 8	206	42.3	12008	17	US-10-776-213-27
C 9	206	42.3	12844	17	US-10-776-213-19
C 10	206	42.3	12850	17	US-10-776-213-22
C 11	206	42.3	12851	17	US-10-776-213-21
C 12	206	42.3	13073	17	US-10-776-213-20
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 29, Appl
					Sequence 23, Appl
					Sequence 25, Appl
					Sequence 26, Appl
					Sequence 24, Appl
					Sequence 21, Appl
					Sequence 19, Appl
					Sequence 22, Appl
					Sequence 21, Appl
					Sequence 20, Appl

C 13	206	42.3	13654	17	US-10-776-213-28
C 14	189.8	39.0	8800	17	US-10-450-097-29
C 15	189.8	39.0	10042	17	US-10-450-097-30
C 16	188.4	38.7	11365	17	US-10-433-311A-17
C 17	176.2	36.2	9952	18	US-10-475-433-10
C 18	120	24.6	1494	18	US-10-475-311-16
C 19	71	14.6	1467	15	US-10-032-585-6216
C 20	62	12.7	312	17	US-10-767-701-26953
C 21	53	10.9	1554	15	US-10-128-714-7070
C 22	53	10.9	1778	15	US-10-128-714-6070
C 23	53	10.9	3140	15	US-10-128-714-70
C 24	53	10.9	3778	15	US-10-128-714-5070
C 25	51	10.5	3673778	15	US-10-312-841-2
C 26	50.6	10.4	467	17	US-10-021-323-6541
C 27	50.6	10.4	3673778	15	US-10-312-841-1
C 28	50.4	10.3	1373	18	US-10-849-901-3
C 29	50.2	10.3	531	17	US-10-021-323-6375
C 30	50.2	10.3	38342	16	US-10-221-714A-471
C 31	50	10.3	6236	15	US-10-311-455-1604
C 32	50	10.3	1830121	14	US-10-329-960-1
C 33	50	10.3	1830121	16	US-10-329-960-1
C 34	50	10.3	1830121	18	US-10-158-865-1
C 35	49.8	10.2	462	18	US-10-425-115-171081
C 36	49.4	10.1	627	13	US-10-027-632-39761
C 37	49.4	10.1	627	15	US-10-027-632-39761
C 38	47.8	9.8	61020	16	US-10-221-714A-513
C 39	47.6	9.8	7047	15	US-10-240-453-260
C 40	47.2	9.7	349	10	US-09-814-353-18039
C 41	47.2	9.7	586	13	US-10-027-632-1415
C 42	47.2	9.7	586	15	US-10-027-632-1415
C 43	47.2	9.7	6308	15	US-10-311-455-1444
C 44	47.2	9.7	8056	18	US-10-473-126-386
C 45	47.2	9.7	9502	16	US-10-221-714A-456

ALIGNMENTS

RESULT 1

US-09-903-508A-3
; Sequence 3, Application US/09903508A
; Publication No. US20030082815A1
; GENERAL INFORMATION:
; APPLICANT: Abbas, Charles
; APPLICANT: Voronovsky, Andrii
; APPLICANT: Kshanovska, Barbara
; APPLICANT: Fayura, Liubov
; APPLICANT: Sibirna, Kateryna
; APPLICANT: Sibirny, Andrii
; APPLICANT: Dmytruk, Kostiantyn
; TITLE OF INVENTION: Transformation Systems for Flavinoogenic Yeast
; FILE REFERENCE: 1533.083003
; CURRENT APPLICATION NUMBER: US/09/903,508A
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,244
; PRIOR APPLICATION NUMBER: US 60/288,491
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/290,667
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Candida famata
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (415) (415)
; OTHER INFORMATION: May be any nucleotide
US-09-903-508A-3

Query Match 99.8% Score 486; DB 10; Length 487;

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OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 20:16:14 ; Search time 2417 Seconds

(without alignments)
7342.222 Million cell updates/sec

Title: US-09-903-508A-3

Perfect score: 487

Sequence: 1 tggattacgaattcgagctcg.....agtttcattgattctgtta 487

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.8	39.0	722	8	AQ639565 927P1-13A
2	92.4	19.0	636	9	CNS06DOK
3	92.4	19.0	1001	9	AL394074 T3 end of
4	88.2	18.1	938	9	AL394073 T7 end of
5	80.4	16.5	903	9	AL403688 T7 end of
6	75.6	15.5	955	9	AL407521 T3 end of
7	62.2	12.8	1027	9	AL430734 clone BA0
8	62	12.7	312	2	AL212733 Tetraodon
9	59.4	12.2	928	9	AW282691 LG1 303 A
10	58.8	12.1	886	8	AL071865 Drosophila
11	58.8	12.1	886	9	BH177277 008_L_22-
12	58.2	12.0	444	8	AL614235 T3 end of
13	57.4	11.8	1020	6	AQ568168 HS 5233 B
14	57.4	11.8	1101	9	CD389622 AGENCOURT
15	57.2	11.7	1045	9	AL069706 Drosophila
16	56.8	11.7	867	9	AL266197 Tetraodon
17	55.4	11.4	970	9	AL060052 Drosophila
18	54.8	11.3	1167	9	AL108800 Drosophila
19	54.6	11.2	753	9	AL427102 clone BA0
20	54.6	11.2	928	9	AG610797 Mus muscu
21	54.4	11.2	987	9	AL071865 Drosophila
22	54.4	11.2	1225	9	AL104456 Drosophila
23	53.6	11.0	935	9	CNS014PQ
24	52.6	10.8	1023	9	CNS0161D
					AL098926 Drosophila
					AL411358 T3 end of

25 52.8 10.8 1101 9 CNS002EM
26 52.8 10.8 1728 3 CR719759 Tetraodon
27 52.6 10.8 524 9 CNS01U90
28 52.4 10.8 878 9 AGS95634 Mus muscu
29 52.4 10.8 893 9 CNS013XE
30 52.4 10.8 973 9 CNS008OF
31 52.4 10.8 1101 9 CNS002FG
32 52.2 10.7 1092 9 CNS020K7
33 52 10.7 581 9 CNS034DK
34 51.8 10.6 1011 9 CNS01510
35 51.8 10.6 1101 9 CNS01611
36 51.6 10.6 911 8 BH161117
37 51.6 10.6 958 9 CNS0074D
38 51.6 10.6 1043 9 CNS0145P
39 51.4 10.6 985 7 CR377065
40 51 10.5 321 1 AU037255
41 51 10.5 646 7 CFS47155
42 51 10.5 1200 9 CNS016CO
43 50.8 10.4 462 4 BM163851
44 50.8 10.4 578 4 BM160131
45 50.8 10.4 931 8 AZ543938

ALIGNMENTS

RESULT 1
AQ639565
LOCUS 722 bp DNA linear GSS 08-JUL-1999
DEFINITION 927P1-13A5.TV 927P1 Trypanosoma brucei genomic clone 927P1-13A5,
genomic survey sequence.
ACCESSION AQ639565
VERSION AQ639565.1 GI:5116275
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE 1 (bases 1 to 722)
AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,
Gerard, C., Leech, V., de Jong, P., Ullu, E., Melville, S.,
Donelson, J., Fraser, C. and Adams, M.
TITLE Determination of clone end sequences from Trypanosoma brucei TREU
927/4 P1 library
JOURNAL Unpublished (1999)
COMMENT Other GSSs: 927P1-13A5.TP
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For clone/filter availability, please contact Sara Melville
(sm160@mol.bio.cam.ac.uk). P1 end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: T7
Class: P1 ends
Location/Qualifiers
1. 722
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927/4"
/db_xref="taxon:5691"
/clone="927P1-13A5"
/clone_lib="927P1"
/note="Vector: pAD10sacBII; Site 1: Bam HI; Constructed by
Sara Melville, University of Cambridge, UK and Nancy
Shepherd, Dupont Merck, Wilmington, DE. Genomic DNA was
isolated from Trypanosoma brucei (stock TREU927/4) and
partially digested with Sau 3A1. DNA fragments were cloned
into the Bam HI site of pAD10sacBII vector (Genbank
accession U09128). The average insert size is 65 Kb.